

SEQUENCE LISTING

(1) GENERAL INFORMATION:



- (i) APPLICANT: O'Brien et al
- (ii) TITLE OF INVENTION: Novel Extracellular Serine Protease
- (iii) NUMBER OF SEQUENCES: 10
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: Benjamin Aaron Adler, Ph.D. J.D.
 - (B) STREET: 8011 Candle Lane
 - (C) CITY: Houston
 - (D) STATE: Texas
 - (E) COUNTRY: USA
 - (F) ZIP: 77071
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: 1.44 Mb floppy disk
 - (B) COMPUTER: Apple Macintosh
 - (C) OPERATING SYSTEM: Macintosh
 - (D) SOFTWARE: Microsoft Word for Macintosh
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER: 08/915,659
 - (B) FILING DATE: August 21, 1997
 - (C) CLASSIFICATION: 435
- (vii) PRIOR APPLICATION DATE:
- (A) APPLICATION NUMBER:
 - (B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Benjamin Aaron Adler, Ph.D.
 - (B) REGISTRATION NUMBER: 35,423
 - (C) REFERENCE/DOCKET NUMBER: D6020
- (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (713) 777-2321
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(2) INFORMATION FOR SEQ ID NO: 1

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 144 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(A) DESCRIPTION: protein

(iii) HYPOTHETICAL: no

(iv) ANTISENSE: no

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(vii) IMMEDIATE SOURCE:

(viii) POSITION IN GENOME:

(ix) FEATURE:

(x) PUBLICATION INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO.: 1

Trp Val Leu Thr Ala Ala His Cys Lys Lys Pro Asn Leu Gln Val
5 10 15
Phe Leu Glu Lys His Asn Leu Arg Gln Arg Glu Ser Ser Gln Glu
20 25 30
Gln Ser Ser Val Val Arg Ala Val Ile His Pro Asp Tyr Asp Ala
35 40 45
Ala Ser His Asp Gln Asp Ile Met Leu Leu Arg Leu Ala Arg Pro
50 55 60
Ala Lys Leu Ser Glu Leu Ile Gln Pro Leu Pro Leu Glu Arg Asp
65 70 75
Cys Ser Ala Asn Thr Thr Ser Cys His Ile Leu Gly Trp Gly Lys
80 85 90

Thr	Ala	Asp	Gly	Asp	Phe	Pro	Asp	Thr	Ile	Gln	Cys	Ala	Tyr	Ile
				95					100					105
His	Leu	Val	Ser	Arg	Glu	Glu	Cys	Glu	His	Ala	Tyr	Pro	Gly	Gln
				110					115					120
Ile	Thr	Gln	Asn	Met	Leu	Cys	Ala	Gln	Asp	Glu	Lys	Tyr	Gly	Lys
				125					130					135
Asp	Ser	Cys	Gln	Gly	Asp	Ser	Gly	Gly						
				140										

(3) INFORMATION FOR SEQ ID NO: 2

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 148 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(A) DESCRIPTION: protein

(iii) HYPOTHETICAL: no

(iv) ANTISENSE: no

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(vii) IMMEDIATE SOURCE:

(viii) POSITION IN GENOME:

(ix) FEATURE:

(x) PUBLICATION INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO.: 2

Trp	Val	Val	Thr	Ala	Ala	His	Cys	Lys	Lys	Pro	Lys	Tyr	Thr	Val
				5					10					15
Arg	Leu	Gly	Asp	His	Ser	Leu	Gln	Asn	Lys	Asp	Gly	Pro	Glu	Gln
				20					25					30
Glu	Ile	Pro	Val	Val	Gln	Ser	Ile	Pro	His	Pro	Cys	Tyr	Asn	Ser
				35					40					45

Ser	Asp	Val	Glu	Asp	His	Asn	His	Asp	Leu	Met	Leu	Leu	Gln	Leu
				50					55					60
Arg	Asp	Gln	Ala	Ser	Leu	Gly	Ser	Lys	Val	Lys	Pro	Ile	Ser	Leu
				65					70					75
Ala	Asp	His	Cys	Thr	Gln	Pro	Gly	Gln	Asn	Cys	Thr	Val	Ser	Gly
				80					85					90
Trp	Gly	Thr	Val	Thr	Ser	Pro	Arg	Glu	Asn	Phe	Pro	Asp	Thr	Leu
				95					100					105
Asn	Cys	Ala	Glu	Val	Lys	Ile	Phe	Pro	Gln	Lys	Lys	Cys	Glu	Asp
				110					115					120
Ala	Tyr	Pro	Gly	Gln	Ile	Thr	Asp	Gly	Met	Val	Cys	Ala	Gly	Ser
				125					130					135
Ser	Lys	Gly	Ala	Asp	Thr	Cys	Gln	Gly	Asp	Ser	Gly	Gly		
				140					145					

(4) INFORMATION FOR SEQ ID NO: 3

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: protein

(iii) HYPOTHETICAL: no

(iv) ANTISENSE: no

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(vii) IMMEDIATE SOURCE:

(viii) POSITION IN GENOME:

(ix) FEATURE:

(x) PUBLICATION INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO.: 3

Trp	Val	Val	Ser	Ala	Gly	His	Cys	Tyr	Lys	Ser	Arg	Ile	Gln	Val
				5					10					15

Arg Leu Gly Glu His Asn Ile Glu Val Leu Glu Gly Asn Glu Gln
 20 25 30
 Phe Ile Asn Ala Ala Lys Ile Ile Arg His Pro Gln Tyr Asp Arg
 35 40 45
 Lys Thr Leu Asn Asn Asp Ile Met Leu Ile Lys Leu Ser Ser Arg
 50 55 60
 Ala Val Ile Asn Ala Arg Val Ser Thr Ile Ser Leu Pro Thr Ala
 65 70 75
 Pro Pro Ala Thr Gly Thr Lys Cys Leu Ile Ser Gly Trp Gly Asn
 80 85 90
 Thr Ala Ser Ser Gly Ala Asp Tyr Pro Asp Glu Leu Gln Cys Leu
 95 100 105
 Asp Ala Pro Val Leu Ser Gln Ala Lys Cys Glu Ala Ser Tyr Pro
 110 115 120
 Gly Lys Ile Thr Ser Asn Met Phe Cys Val Gly Phe Leu Glu Gly
 125 130 135
 Gly Lys Asp Ser Cys Gln Gly Asp Ser Gly Gly
 140 145

(5) INFORMATION FOR SEQ ID NO: 4

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 144 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(A) DESCRIPTION: protein

(iii) HYPOTHETICAL: no

(iv) ANTISENSE: no

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(vii) IMMEDIATE SOURCE:

(viii) POSITION IN GENOME:

(ix) FEATURE:

(x) PUBLICATION INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO.: 4

Trp Val Leu Thr Ala Ala His Cys Lys Met Asn Glu Tyr Thr Val
5 10 15
His Leu Gly Ser Asp Thr Leu Gly Asp Arg Arg Ala Gln Arg Ile
20 25 30
Lys Ala Ser Lys Ser Phe Arg His Pro Gly Tyr Ser Thr Gln Thr
35 40 45
His Val Asn Asp Leu Met Leu Val Lys Leu Asn Ser Gln Ala Arg
50 55 60
Leu Ser Ser Met Val Lys Lys Val Arg Leu Pro Ser Arg Cys Glu
65 70 75
Pro Pro Gly Thr Thr Cys Thr Val Ser Gly Trp Gly Thr Thr Thr
80 85 90
Ser Pro Asp Val Thr Phe Pro Ser Asp Leu Met Cys Val Asp Val
95 100 105
Lys Leu Ile Ser Pro Gln Asp Cys Thr Lys Val Tyr Lys Asp Leu
110 115 120
Leu Glu Asn Ser Met Leu Cys Ala Gly Ile Pro Asp Ser Lys Lys
125 130 135
Asn Ala Cys Asn Gly Asp Ser Gly Gly
140

(6) INFORMATION FOR SEQ ID NO: 5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(A) DESCRIPTION: protein

(iii) HYPOTHETICAL: no

- (iv) ANTISENSE: no
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
- (vii) IMMEDIATE SOURCE:
- (viii) POSITION IN GENOME:
- (ix) FEATURE:
- (x) PUBLICATION INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO.: 5

Trp Val Leu Thr Ala Ala His Cys Phe Pro Glu Arg Asn Arg Val
 5 10 15
 Leu Ser Arg Trp Arg Val Phe Ala Gly Ala Val Ala Gln Ala Ser
 20 25 30
 Pro His Gly Leu Gln Leu Gly Val Gln Ala Val Val Tyr His Gly
 35 40 45
 Gly Tyr Leu Pro Phe Arg Asp Pro Asn Ser Glu Glu Asn Ser Asn
 50 55 60
 Asp Ile Ala Leu Val His Leu Ser Ser Pro Leu Pro Leu Thr Glu
 65 70 75
 Tyr Ile Gln Pro Val Cys Leu Pro Ala Ala Gly Gln Ala Leu Val
 80 85 90
 Asp Gly Lys Ile Cys Thr Val Thr Gly Trp Gly Asn Thr Gln Tyr
 95 100 105
 Tyr Gly Gln Gln Ala Gly Val Leu Gln Glu Ala Arg Val Pro Ile
 110 115 120
 Ile Ser Asn Asp Val Cys Asn Gly Ala Asp Phe Tyr Gly Asn Gln
 125 130 135
 Ile Lys Pro Lys Met Phe Cys Ala Gly Tyr Pro Glu Gly Gly Ile
 140 145 150
 Asp Ala Cys Gln Gly Asp Ser Gly Gly
 155

(7) INFORMATION FOR SEQ ID NO: 6

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1343 bp

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: single-stranded
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(A) DESCRIPTION: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTISENSE: no

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(vii) IMMEDIATE SOURCE:

(viii) POSITION IN GENOME:

(ix) FEATURE:

(x) PUBLICATION INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO.: 6

CTGTAGCAGG	CAGAGCTTAC	CAAGTCTCTC	CGAACTCAAA	TGGAAGAAAT	ACCTTATGAA	60
TGTAAGAATG	TAGGGGGTCA	TGGCTTGTA	TTTACACAGT	GTAAATGAAA	CCATCCTAGA	120
GGATTATGAG	GAATCCTTTC	TATGTGATTT	TCAATCATAG	CAAGCAAGAA	AGGCTCCAGT	180
GTCAAGGTAG	TTCAGCTCTT	ACAGGATATA	AAACAGTCCA	TACTTGAGAG	AAAAAACTTA	240
GATCTGAGTG	ATGGAATGTG	AAGCAAATCT	TTCAAAATCA	GTAGACATTT	CTTGGACATA	300
AAACACAGAT	GAGGAAAGGG	CTTCAAATTA	GAAGTTACGT	AATCACCATC	AGAAAGTTCA	360
TGTTTGGTAA	ATTCTGTTAC	TAGAAATGTA	GGAAATTCAG	GTATAGCTTT	GAATCCCAAT	420
TACACATTGG	TCAGTGGGAA	AACTAAGGGC	CTCCAACAGG	CAAATTCAGG	GAGGATAGGT	480
TTCAGGGAAT	GCCCTGGATT	CTGGAAGACC	TCACCATGGG	ACGCCCCCGA	CCTCGTGCGG	540
CCAAGACGTG	GATGTTCTTG	CTCTTGCTGG	GGGGAGCCTG	GGCAGGACAC	TCCAGGGCAC	600
AGGAGGACAA	GGTGCTGGGG	GGTCATGAGT	GCCAACCCCA	TTCGCAGCCT	TGGCAGGCGG	660
CCTTGTTCCA	GGGCCAGCAA	CTACTCTGTG	GCGGTGTCTT	TGTAGGTGGC	AACTGGGTCC	720
TTACAGCTGC	CCACTGTAAA	AAACCGAAAT	ACACAGTACG	CCTGGGAGAC	CACAGCCTAC	780
AGAATAAAGA	TGGCCCAGAG	CAAGAAATAC	CTGTGGTTCA	GTCCATCCCA	CACCCCTGCT	840
ACAACAGCAG	CGATGTGGAG	GACCACAACC	ATGATCTGAT	GCTTCTTCAA	CTGCGTGACC	900
AGGCATCCCT	GGGGTCCAAA	GTGAAGCCCA	TCAGCCTGGC	AGATCATTGC	ACCCAGCCTG	960
GCCAGAAGTG	CACCGTCTCA	GGCTGGGGCA	CTGTCACCAG	TCCCCGAGAG	AATTTTCCTG	1020
ACACTCTCAA	CTGTGCAGAA	GTAAAAATCT	TTCCCCAGAA	GAAGTGTGAG	GATGCTTACC	1080
CGGGGCAGAT	CACAGATGGC	ATGGTCTGTG	CAGGCAGCAG	CAAAGGGGCT	GACACGTGCC	1140
AGGGCGATTG	TGGAGGCCCC	CTGGTGTGTG	ATGGTGCAC	CCAGGGCATC	ACATCCTGGG	1200
GCTCAGACCC	CTGTGGGAGG	TCCGACAAAC	CTGGCGTCTA	TACCAACATC	TGCCGCTACC	1260
TGGACTGGAT	CAAGAAGATC	ATAGGCAGCA	AGGGCTGATT	CTAGGATAAG	CACTAGATCT	1320
CCCTTAATAA	ACTCACGGAA	TTC				1343

(8) INFORMATION FOR SEQ ID NO: 7

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 260 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(A) DESCRIPTION: protein

(iii) HYPOTHETICAL: no

(iv) ANTISENSE: no

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(vii) IMMEDIATE SOURCE:

(viii) POSITION IN GENOME:

(ix) FEATURE:

(x) PUBLICATION INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO.: 7

Met Gly Arg Pro Arg Pro Arg Ala Ala Lys Thr Trp Met Phe Leu
5 10 15
Leu Leu Leu Gly Gly Ala Trp Ala Gly His Ser Arg Ala Gln Glu
20 25 30
Asp Lys Val Leu Gly Gly His Glu Cys Gln Pro His Ser Gln Pro
35 40 45
Trp Gln Ala Ala Leu Phe Gln Gly Gln Gln Leu Leu Cys Gly Gly
50 55 60
Val Leu Val Gly Gly Asn Trp Val Leu Thr Ala Ala His Cys Lys
65 70 75
Lys Pro Lys Tyr Thr Val Arg Leu Gly Asp His Ser Leu Gln Asn
80 85 90
Lys Asp Gly Pro Glu Gln Glu Ile Pro Val Val Gln Ser Ile Pro
95 100 105
His Pro Cys Tyr Asn Ser Ser Asp Val Glu Asp His Asn His Asp
110 115 120
Leu Met Leu Leu Gln Leu Arg Asp Gln Ala Ser Leu Gly Ser Lys
125 130 135

Val Lys Pro Ile Ser Leu Ala Asp His Cys Thr Gln Pro Gly Gln
140 145 150

Lys Cys Thr Val Ser Gly Trp Gly Thr Val Thr Ser Pro Arg Glu
155 160 165

Asn Phe Pro Asp Thr Leu Asn Cys Ala Glu Val Lys Ile Phe Pro
170 175 180

Gln Lys Lys Cys Glu Asp Ala Tyr Pro Gly Gln Ile Thr Asp Gly
185 190 195

Met Val Cys Ala Gly Ser Ser Lys Gly Ala Asp Thr Cys Gln Gly
200 205 210

Asp Ser Gly Gly Pro Leu Val Cys Asp Gly Ala Leu Gln Gly Ile
215 220 225

Thr Ser Trp Gly Ser Asp Pro Cys Gly Arg Ser Asp Lys Pro Gly
230 235 240

Val Tyr Thr Asn Ile Cys Arg Tyr Leu Asp Trp Ile Lys Lys Ile
245 250 255

Ile Gly Ser Lys Gly
260

(9) INFORMATION FOR SEQ ID NO: 8

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 bp
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single-stranded
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: other nucleic acid

(iii) HYPOTHETICAL: no

(iv) ANTISENSE: no

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(vii) IMMEDIATE SOURCE:

(viii) POSITION IN GENOME:

46

(ix) FEATURE:

(x) PUBLICATION INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO.: 8

AGAGGCCACC	ATGGGACGCC	CCCCACCCTG	TGCAATCCAG	CCGTGGATCC	TTCTGCTTCT	60
GTTCATGGGA	GCGTGGGCAG	GGCTCACCAG	AGCTCAGGGC	TCCAAGATCC	TGGAAGGTCG	120
AGAGTGTATA	CCCCACTCCC	AGCCTTGGCA	GGCAGCCTTG	TTCCAGGGCG	AGAGACTGAT	180
CTGTGGGGGT	GTCCTGGTTG	GAGACAGATG	GGTCCTCACG	GCAGCCCACT	GCAAAAAACA	240
GAAGTACTCC	GTGCGTCTGG	GTGATCATAG	CCTCCAGAGC	AGAGATCAGC	CGGAGCAGGA	300
GATCCAGGTG	GCTCAGTCTA	TCCAGCATCC	TTGCTACAAC	AACAGCAACC	CAGAAGATCA	360
CAGTCACGAT	ATAATGCTCA	TTCGACTGCA	GAATCAGCA	AACCTCGGGG	ACAAGGTGAA	420
GCCGGTCCAA	CTGGCCAATC	TGTGTCCCAA	AGTTGGCCAG	AAGTGCATCA	TATCAGGCTG	480
GGGCACTGTC	ACCAGCCCTC	AAGAGAACTT	TCCAAACACC	CTCAACTGTG	CGGAAGTGAA	540
AATCTATTCC	CAGAACAAGT	GTGAGAGAGC	CTATCCAGGG	AAGATCACCG	AGGGCATGGT	600
CTGTGCTGGC	AGCAGCAATG	GAGCTGACAC	GTGCCAGGGT	GACTCAGGAG	GCCCTCTGGT	660
GTGCGACGGG	ATGCTCCAGG	GCATCACCTC	ATGGGGCTCA	GACCCCTGTG	GGAAACCCGA	720
GAAACCTGGA	GTCTACACCA	AAATCTGCCG	CTACACTACC	TGGATCAAGA	AGACCATGGA	780
CAACAGGGAC	TGATCCTGG					799

(10) INFORMATION FOR SEQ ID NO: 9

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 799 bp

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single-stranded

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(A) DESCRIPTION: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTISENSE: no

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(vii) IMMEDIATE SOURCE:

(viii) POSITION IN GENOME:

(ix) FEATURE:

(x) PUBLICATION INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO.: 9

AGACCTCACC	ATGGGACGCC	CCCGACCTCG	TGCGGCCAAG	ACGTGGATGT	TCCTGCTCTT	60
GCTGGGGGGA	GCCTGGGCAG	GACACTCCAG	GGCACAGGAG	GACAAGGTGC	TGGGGGGTCA	120

TGAGTGCCAA	CCCCATTCGC	AGCCTTGGA	GGCGGCCTTG	TTCCAGGGCC	AGCAACTACT	180
CTGTGGCGGT	GTCCTGTAG	GTGGCAACTG	GGTCCTTACA	GCTGCCCCACT	GTAAAAAACC	240
GAAATACACA	GTACGCCTGG	GAGACCACAG	CCTACAGAAT	AAAGATGGCC	CAGAGCAAGA	300
AATACCTGTG	GTTTCAGTCCA	TCCCACACCC	CTGCTACAAC	AGCAGCGATG	TGGAGGACCA	360
CAACCATGAT	CTGATGCTTC	TTCAACTGCG	TGACCAGGCA	TCCCTGGGGT	CCAAAGTGAA	420
GCCCATCAGC	CTGGCAGATC	ATTGCACCCA	GCCTGGCCAG	AAGTGCACCG	TCTCAGGCTG	480
GGGCACTGTC	ACCAGTCCCC	GAGAGAATTT	TCCTGACACT	CTCAACTGTG	CAGAAGTAAA	540
AATCTTTCCC	CAGAAGAAGT	GTGAGGATGC	TTACCCGGGG	CAGATCACAG	ATGGCATGGT	600
CTGTGCAGGC	AGCAGCAAAG	GGGCTGACAC	GTGCCAGGGC	GATTCTGGAG	GCCCCCTGGT	660
GTGTGATGGT	GCACTCCAGG	GCATCACATC	CTGGGGCTCA	GACCCCTGTG	GGAGGTCCGA	720
CAAACCTGGC	GTCTATACCA	ACATCTGCCG	CTACCTGGAC	TGGATCAAGA	AGATCATAGG	780
CAGCAAGGGC	TGATTCTAG					799

(11) INFORMATION FOR SEQ ID NO: 10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 260 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(A) DESCRIPTION: protein

(iii) HYPOTHETICAL: no

(iv) ANTISENSE: no

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(vii) IMMEDIATE SOURCE:

(viii) POSITION IN GENOME:

(ix) FEATURE:

(x) PUBLICATION INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO.: 10

Met	Gly	Arg	Pro	Pro	Pro	Cys	Ala	Ile	Gln	Pro	Trp	Ile	Leu	Leu
				5					10					15
Leu	Leu	Phe	Met	Gly	Ala	Trp	Ala	Gly	Leu	Thr	Arg	Ala	Gln	Gly
				20					25					30
Ser	Lys	Ile	Leu	Glu	Gly	Arg	Glu	Cys	Ile	Pro	His	Ser	Gln	Pro
				35					40					45

Trp Gln Ala Ala Leu Phe Gln Gly Glu Arg Leu Ile Cys Gly Gly
 50 55 60
 Val Leu Val Gly Asp Arg Trp Val Leu Thr Ala Ala His Cys Lys
 65 70 75
 Lys Gln Lys Tyr Ser Val Arg Leu Gly Asp His Ser Leu Gln Ser
 80 85 90
 Arg Asp Gln Pro Glu Gln Glu Ile Gln Val Ala Gln Ser Ile Gln
 95 100 105
 His Pro Cys Tyr Asn Asn Ser Asn Pro Glu Asp His Ser His Asp
 110 115 120
 Ile Met Leu Ile Arg Leu Gln Asn Ser Ala Asn Leu Gly Asp Lys
 125 130 135
 Val Lys Pro Val Gln Leu Ala Asn Leu Cys Pro Lys Val Gly Gln
 140 145 150
 Lys Cys Ile Ile Ser Gly Trp Gly Thr Val Thr Ser Pro Gln Glu
 155 160 165
 Asn Phe Pro Asn Thr Leu Asn Cys Ala Glu Val Lys Ile Tyr Ser
 170 175 180
 Gln Asn Lys Cys Glu Arg Ala Tyr Pro Gly Lys Ile Thr Glu Gly
 185 190 195
 Met Val Cys Ala Gly Ser Ser Asn Gly Ala Asp Thr Cys Gln Gly
 200 205 210
 Asp Ser Gly Gly Pro Leu Val Cys Asp Gly Met Leu Gln Gly Ile
 215 220 225
 Thr Ser Trp Gly Ser Asp Pro Cys Gly Lys Pro Glu Lys Pro Gly
 230 235 240
 Val Tyr Thr Lys Ile Cys Arg Tyr Thr Thr Trp Ile Lys Lys Thr
 245 250 255
 Met Asp Asn Arg Asp
 260